"Replacement Sheet

FIG. 4B-8

helicase-moi	BF590131	2.21
Consensus Includes gb:R06655 /FEA=EST /DB_XREF=gi:75	7275	
/DB_XREF=est:yf10e02.r1 /CLONE=IMAGE:126458		
/UG=Hs.188518 ESTs, Moderately similar to AF078844 1 hqp		
protein H.sapiens	R06655	2.21
hypothetical protein FLJ23311	NM_024680	2.21
xylulokinase (H. influenzae) homolog	AA777793	2.21
islet cell autoantigen 1 (69kD)	BC005922	2.20
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin		
synthetase corresponding to nucleotides 2071-2304 of J04423		
/LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Micand 3 prime respectively)		0.00
and 3 prime respectively)	J04423	2.20
degenerative spermatocyte homolog, lipid desaturase (Drosop	•	2.20
high-mobility group 20B	BC002552	2.19
Consensus includes gb:Al984051 /FEA=EST /DB_XREF=gi:5811270 /DB_XREF=est:wt52h03.x1		
/CLONE=IMAGE:2511125 /UG=Hs.11861 thyroid hormone	•	
receptor-associated protein, 240 kDa subunit /FL=gb:AF11775	4 1	
gb:NM_005121.1	Al984051	2.19
Consensus includes gb:Al683552 /FEA=EST		
/DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1		
/CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately	•	
similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE	•	
CONTAMINATION WARNING ENTRY H.sapiens	Al683552	2.19
Consensus includes gb:Al393960 /FEA=EST		
/DB_XREF=gi:4223507 /DB_XREF=est:tg11d04.x1 /CLONE=IMAGE:2108455 /UG=Hs.274851 ESTs	Al393960	2.40
CGI-58 protein		2.19
PDZ domain containing guanine nucleotide exchange	NM_016006	2.19
factor(GEF)1	AV654984	2.18
hypothetical protein FLJ12985	NM_024924	2.18
SHB adaptor protein (a Src homology 2 protein)	NM_003028	2.18
WNT1 inducible signaling pathway protein 3	AF143679	2.17
hypothetical protein FLJ20274	NM_017736	2.17
solute carrier family 16 (monocarboxylic acid transporters),	14141_017730	4.17
member 7	NM_004731	2.17
Consensus includes gb:AA780524 /FEA=EST	· · · · · _ · · · · · · · · · · · · · ·	
/DB_XREF=gi:2839855 /DB_XREF=est:ac71f01.s1		
/CLONE=IMAGE:868057 /UG=Hs.294072 ESTs, Weakly simila	r to	
ALU1_HUMAN ALU SUBFAMILY J SEQUENCE		
CONTAMINATION WARNING ENTRY H.sapiens	AA780524	2.17
hypothetical protein FLJ12619	BG252842	2.17
M10098 Human 18S rRNA gene, complete (_5, _M, _3 represe		
transcript regions 5 prime, Middle, and 3 prime respectively)	M10098	2.17
J04423 E coli bioC protein (-5 and -3 represent transcript region		
5 prime and 3 prime respectively)	J04423	2.17
coat protein gamma-cop	NM_016128	2.16
a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	NIM 003493	2.46
ring finger protein 2	NM_003183	2.16
ring inigal protein z	NM_007212	2.16